

Exhibit A**BLAST****Basic Local Alignment Search Tool**[Edit and Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

SEQ ID NO:1 vs. XM_044533Results for: 46661 None(837aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID 46661
 46661**Description**

None

Molecule type

amino acid

Query Length

837

Subject ID

46663

Description

None

Molecule type

amino acid

Subject Length

837

ProgramBLASTP 2.2.23+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Multiple alignment](#)]

[Search Parameters](#)**Search parameter name** **Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1

Matrix BLOSUM62
 Filter string F
 Genetic Code 1
 Window Size 40
 Threshold 11
 Composition-based stats 2

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320342	0.267
K	0.136493	0.041
H	0.42551	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

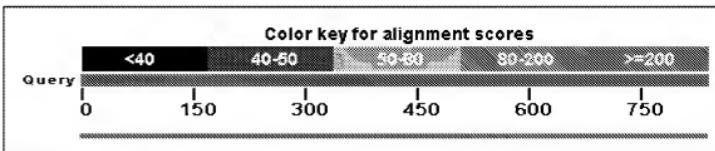
Effective search space	632025
------------------------	--------

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Dot Matrix View

Plot of Icl|46661 vs 46663 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
46663	unnamed protein product	1698	1698	100%	0.0	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>Icl|46663 unnamed protein product
Length=837

```
Score = 1698 bits (4398), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 831/837 (99%), Positives = 831/837 (99%), Gaps = 0/837 (0%)
Query 1      MLRTAMGLRSWLAAPWGALPAPRPPPLLLLLLQLPPPTWALSPrISLPLGSEERPFL 60
Sbjct 1      MLRTAMGLRSWLAAPWGALPAPRPPPLLLLLLQLPPPTWALSPrISLPLGSEERPFL 60
Query 61     RFEAEHISNYTALLLSRDGRTLVYVGAREALFALSSNLsFLPGGEYQELLWGADEAKKKQC 120
Sbjct 61     RFEAEHISNYTALLLSRDGRTLVYVGAREALFALSSNLsFLPGGEYQELLWGADEAKKKQC 120
Query 121    SFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINNMENFTLARDEKGKVNLLED 180
Sbjct 121    SFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINNMENFTLARDEKGKVNLLED 180
Query 181    GKGRCPFDPNFKSTALVVVDGELYTGTVSSFQGNDPAISRSQSRLPTKTESSLNWLQDPAF 240
Sbjct 181    GKGRCPFDPNFKSTALVVVDGELYTGTVSSFQGNDPAISRSQSRLPTKTESSLNWLQDPAF 240
Query 241    VASAYIPESLGLSLQGDDDKIYFFFSETGQEFFECTIVSRARIICKGDEGGERVLQQRW 300
Sbjct 241    VASAYIPESLGLSLQGDDDKIYFFFSETGQEFFECTIVSRARIICKGDEGGERVLQQRW 300
Query 301    TSFLKAQLLCSRDPDGFPNVLQDVFTLSPSPQDWRTDLYFGVTSQWHRGTTGEAVCV 360
Sbjct 301    TSFLKAQLLCSRDPDGFPNVLQDVFTLSPSPQDWRTDLYFGVTSQWHRGTTGEAVCV 360
Query 361    FTMKDQVRVFSGLYKEVNRETQQMVHRRDPVPTRPGACITNSARERKINSSLQLPDRVL 420
Sbjct 361    FTMKDQVRVFSGLYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVL 420
```

Query	421	NFLKDHFILMDGQVRSRMILLQPOQARYQRVAVHRVPGLHHHTYDVLFLGTGDGRLLHKAVSVG	480
Sbjct	421	NFLKDHFILMDQVRSRMILLQPOQARYQRVAVHRVPGLHHHTYDVLFLGTGDGRLLHKAVSVG	480
Query	481	PRVHIIIEELQIFSSGQPVQNLLLDTHRGGLYAAASHSGVVQPMANCSLYRSCGDCLLARD	540
Sbjct	481	PRVHIIIEELQIFSSGQPVQNLLLDTHRGGLYAAASHSGVVQPMANCSLYRSCGDCLLARD	540
Query	541	PYCAGWSGSSCKHVSLYQPQLATRPWIQDIEGAGAKDLCSASSVSPSFVPTGEKPCEQVQ	600
Sbjct	541	PYCAGWSGSSCKHVSLYQPQLATRPWIQDIEGAGAKDLCSASSVSPSFVPTGEKPCEQVQ	600
Query	601	FQPNTVNLACPLLSNLTALTRLWLRNGAPVNASASCHVLPTGDLLLVGTQQLGEFQCWSLE	660
Sbjct	601	FQPNTVNLACPLLSNLTALTRLWLRNGAPVNASASCHVLPTGDLLLVGTQQLGEFQCWSLE	660
Query	661	EGFQQLVASYCPEVVEDGVADQTDEGGSVFVIIISTSRVSAFAGGKASWGADRSYWKEFLV	720
Sbjct	661	EGFQQLVASYCPEVVEDGVADQTDEGGSVFVIIISTSRVSAFAGGKASWGADRSYWKEFLV	720
Query	721	MCTLFVLAVLVPVLFLYRRHNSMKVFLQGECASVHPKTCPPVLPETRPLNGLGPST	780
Sbjct	721	MCTLFVLAVLVPVLFLYRRHNSMKVFLQGECASVHPKTCPPVLPETRPLNGLGPST	780
Query	781	PLDHRGYQSLSDSPPGSRVFTESERKRLPSIQDSFVEVSPVCPRPRVRLGSEIRDSSV	837
Sbjct	781	PLDHRGYQSLSDSPPGSRVFTESERKRLPSIQDSFVEVSPVCPRPRVRLGSEIRDSSV	837

Select All Get selected sequences Distance tree of results Multiple alignment